

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences
City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use
of a
structure of a complex between a TRF2 DNA binding domain and a double-stranded
DNA molecule

<130> FP-047PCT

<140> 10/590,464

<141> 2006-08-23

<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<213> Homo sapiens

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Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
 Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
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atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
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gaa gag gca gtc aat cgc tgg gtg etc aag ttc tac ttc cac gag cgc 192
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Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg
65 70 75 80

gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc 288
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr
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Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
100 105 110

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Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro

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Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys			
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	180	185	190
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Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu			
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Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro			
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Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu			
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Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala			
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cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac			1008
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385 390 395 400

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50 55 60

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Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu
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265

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